



(1) GENERAL INFORMATION:

(i) APPLICANTS: Gaugler, B*atrice; Van den Eynde, Benoit; van der Bruggen, Pierre; Boon-Falleur, Thierry

(ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
- (B) STREET: 666 Fifth Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (F) ZIP: 10103

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/579,543
- (B) FILING DATE: 26-MAY-2000
- (C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/583,850
- (B) FILING DATE: 30-May-2000

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US92/04354
- (B) FILING DATE: 22-MAY-1992

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/807,043
- (B) FILING DATE: 12-DECEMBER-1991

(ix) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/764,364
- (B) FILING DATE: 23-SEPTEMBER-1991

(x) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/728,838
- (B) FILING DATE: 9-JULY-1991

(xi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/705,702
- (B) FILING DATE: 23-MAY-1991

(xii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Hanson, Norman D.
- (B) REGISTRATION NUMBER: 30,946
- (C) REFERENCE/DOCKET NUMBER: LUD 5353.5 DIV (10016355)

(xiii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 688-9200

(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG      60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT    120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG    180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC    240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT    300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT    360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT    420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                        462
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(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
      5                      10                      15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
      20                      25                      30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA    144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
      35                      40                      45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG    192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
      50                      55                      60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC    240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
      65                      70                      75                      80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC    288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
      85                      90                      95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT    336
Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
      100                      105                      110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG    384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
      115                      120                      125
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GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met	
130 135 140	
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys	
145 150 155 160	
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe	
165 170 175	
CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys	
180 185 190	
GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG	624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu	
195 200 210	
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro	
220 225 230 235	
TAG	675

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT	60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT	120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC	180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC	228

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1365 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
TAT TTC TAT CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTTAAAAATA AAAGTTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGTTGGT GGGTCATTGC	1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066

CCCCACTCCT	TGCTCCGCTC	TCTTTCCCTT	TCCCACCTTG	CCTCTGGAGC	1116
TTCAGTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTTGCTCTC	CTTGCTCCCC	1166
TCCCCCTCGG	CTCAACTTTT	CGTGCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
TTCAGGCTTC	CCCATTTGCT	CCTCTCCCGA	AACCCTCCCC	TTCCTGTTCC	1266
CCTTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCTGGCAC	1616
TCACTCTGTA	GACCAGGCT	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916
GCCCCGTTC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
AGCTCACCTT	TTTGTGTTGT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCCTCCCC	TCCGGCTTCC	2066
CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCC	TCGCTGGCTC	CCCCCTCCCT	2116
TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA	CTCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG	CTCCCCCTCC	CCTCCCAGCT	CCCCCTCTT	TTCCCACCTC	2266
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCCT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCCT	2466
ATGTGTCTCT	CTTCTATCT	ATCCCTTCC	TTCTGTCCCC	TCTCCTCTGT	2516
CCATCACCCT	TCTCCTCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATG	CCCTCTACTC	2766
TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAA	ATCAGCAGGA	2916
AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
TTGCTAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355
GT GTT CCT	GGC CAT CAT	TTA AGG	AAG AAT GAA	GTG AAG TGT	3396
AGG ATG ATT	TAT TTC TTC	CAC GAC	CCT AAT TTC	CTG GTG TCT	3438
ATA CCA GTG	AAC CCT AAG	GAA CAA	ATG GAG TGT	AGG TGT GAA	3480
AAT GCT GAT	GAA GAG GTT	GCA ATG	GAA GAG GAA	GAA GAA GAA	3522
GAG GAG GAG	GAG GAG GAA	GAG GAA	ATG GGA AAC	CCG GAT GGC	3564
TTC TCA CCT	TAG				3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
GCTAAGAGCA	TCTTTTTTAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826

GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCTG	3976
TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
CTTAAATTTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTCACT	4076
TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTTA	GATTTCTTAA	4126
AATGTTTTTT	AAAAAAAATG	CAAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
GTAAGTGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
AGTCAGGAGT	GTATTCTAAT	AAGTGTGTCT	TATCTCTTAT	TTTCTTCTAC	4476
AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576
TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
AATAAAAGTT	TGACTTGCAT	AC			4698

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe

5

(2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCTCTTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCTCCTTTC	AGGTTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCACTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800

AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCTCTGA	1050
GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCCG	ACAGTGATCC	1400
CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT	CCCTGCGTGA	AGCAGCTTTG	AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA	AGGCCAGTGG	GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG	AGATTTATCT	TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAGG	GATGGTTGAA	TGAACTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTGTT	TTATTTCAGAT	TGGGAAATCC	ATTCTATTTT	GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA	AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCCTTG	2000
CTTATACCTC	AGTCTATTCT	GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050
GATTTCCCTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCCTCCT	GTTCACATGG	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2419

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCCGGGCAC	CACTGGCATC	CCTCCCCCTA	CCACCCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550

ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCATT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCCTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTTCCG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
CGCGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAAATC	CCATCTCCAC	CCCATTTCGA	TTCCCATTC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTTCT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAAGTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACTT	ACCCCTTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCATCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTGAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCCAG	GACCAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCTCCT	GTCTTCCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400

CTGAGGGCCC	GTGGATTCCT	CTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
ATCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
TCCCTCTCTC	CCCAGGCCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCCACA	3850
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG	CCT GAG GAA	3922
GCC CTT GAG	GCC CAA CAA	GAG GGC	CTG GGC	CTG GTG TGT	3964
CAG GCT GCC	ACC TCC TCC	TCC TCT CCT	CTG GTC	CTG GGC ACC	4006
CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT	CCT CCC CAG	4048
AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC	ATC AAC TTC	4090
ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC	AGC CGT GAA	4132
GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG	TCC TTG TTC	4174
CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG	GTT GGT TTT	4216
CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC	ACA AAG GCA	4258
GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG	CAC TGT TTT	4300
CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG	CAG CTG GTC	4342
TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC	GGC CAC TCC	4384
TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT	GAT GGC CTG	4426
CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC	TTC CTG ATA	4468
ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC	CAT GCT CCT	4510
GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG	GAG GTG TAT	4552
GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC	AGG AAG CTG	4594
CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG	GAG TAC GGC	4636
AGG TGC CGG	ACA GTG ATC	CCG CAC GCT	ATG AGT	TCC TGT GGG	4678
GTC CAA GGG	CCC TCG CTG	AAA CCA GCT	ATG TGA		4711
AAGTCCTTGA	GTATGTGATC	AAGGTCAGTG	CAAGAGTTC		4750
GCTTTTTCTT	CCCATCCCTG	CGTGAAGCAG	CTTTGAGAGA	GGAGGAAGAG	4800
GGAGTCTGAG	CATGAGTTGC	AGCCAAGGCC	AGTGGGAGGG	GGACTGGGCC	4850
AGTGCACCTT	CCAGGGCCGC	GTCCAGCAGC	TTCCCCTGCC	TCGTGTGACA	4900
TGAGGCCCAT	TCTTCACTCT	GAAGAGAGCG	GTCAGTGTTT	TCAGTAGTAG	4950
GTTTCTGTTC	TATTGGGTGA	CTTGGAGATT	TATCTTTGTT	CTCTTTTGGG	5000
ATTGTTCAAA	TGTTTTTTTT	TAAGGGATGG	TTGAATGAAC	TTCAGCATCC	5050
AAGTTTATGA	ATGACAGCAG	TCACACAGTT	CTGTGTATAT	AGTTTAAGGG	5100
TAAGAGTCTT	GTGTTTTATT	CAGATTGGGA	AATCCATTCT	ATTTTGTGAA	5150
TTGGGATAAT	AACAGCAGTG	GAATAAGTAC	TTAGAAATGT	GAAAAATGAG	5200
CAGTAAAATA	GATGAGATAA	AGAATAAG	AAATTAAGAG	ATAGTCAATT	5250
CTTGCCTTAT	ACCTCAGTCT	ATTCTGTAAA	ATTTTAAAG	ATATATGCAT	5300
ACCTGGATTT	CCTTGGCTTC	TTTGAGAAATG	TAAGAGAAAT	TAAATCTGAA	5350
TAAAGAATTC	TTCTGTTC	CTGGCTCTTT	TCTTCTCCAT	GCACTGAGCA	5400
TCTGCTTTTT	GGAAGGCCCT	GGTTAGTAG	TGGAGATGCT	AAGGTAAGCC	5450
AGACTCATAC	CCACCCATAG	GGTCGTAGAG	TCTAGGAGCT	GCAGTCACGT	5500
AATCGAGGTG	GCAAGATGTC	CTCTAAAGAT	GTAGGGAAAA	GTGAGAGAGG	5550
GGTGAGGGTG	TGGGGCTCCG	GGTGAGAGTG	GTGGAGTGTC	AATGCCCTGA	5600
GCTGGGGCAT	TTTGGGCTTT	GGGAACTGC	AGTTCCTTCT	GGGGGAGCTG	5650
ATTGTAATGA	TCTTGGGTGG	ATCC			5674

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(ix) FEATURE:
(A) NAME/KEY: MAGE-2 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCACCCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCTG	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACCTCTG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCTTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCTG	TACCCCTGTC	800
TCAAACCTGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCGGCCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTT	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTTCAGGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCAACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCTG	CAGATGCAGT	GGTTCCTAGG	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
GTCTTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACCTGAAGG	CCGTGCATT	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550

CCCAGCTCCT	GCCCCGACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
ATA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
TTG AGA GAG	GGA GAA GAG	TGA			3542
GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATTCT	TAGCAGTGAG	3692
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
TTGTTCAAAT	GTTCCTTTTA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
TTTTATGAAT	GACATAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
TAAGAGTCCT	GTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
TTGTCACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCTAT	ATTGTGAACG	3942
AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
TCACTGGCTC	ATTTCTTTAC	CATTCACTCA	GCATCTGCTC	TGTGGAAGGC	4142
CCTGGTAGTA	GTGGG				4157

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350

CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1640 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG	AAGCCGGCCC	AGGCTCGGTG	AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA	CCTGGAGGAC	CAGAGGCCCC	CGGAGGAGCA	CTGAAGGAGA	100
AGATCTGCCA	GTGGGTCTCC	ATTGCCCAGC	TCCTGCCAC	ACTCCCGCCT	150
GTTGCCCTGA	CCAGAGTCAT	C			171
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	213
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	255
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	297
TCT ACT CTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	339
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	381
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	423
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	465
CCT GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	507
GTG GCC GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	549
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GGG AGT	GTC GTC	591
GGA AAT TGG	CAG TAT TTC	TTT CCT GTG	ATC TTC AGC	AAA GCT	633
TCC AGT TCC	TTG CAG CTG	GTC TTT GGC	ATC GAG CTG	ATG GAA	675
GTG GAC CCC	ATC GGC CAC	TTG TAC ATC	TTT GCC ACC	TGC CTG	717
GGC CTC TCC	TAC GAT GGC	CTG CTG GGT	GAC AAT CAG	ATC ATG	759
CCC AAG GCA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	801
AGA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	843
CTG AGT GTG	TTA GAG GTG	TTT GAG GGG	AGG GAA GAC	AGT ATG	885
TTG GGG GAT	CCC AAG AAG	CTG CTC ACC	CAA CAT TTC	GTG CAG	927
GAA AAC TAC	CTG GAG TAC	CGG CAG GTC	CCC GGC AGT	GAT CCT	969
GCA TGT TAT	GAA TTC CTG	TGG GGT CCA	AGG GCC CTC	GTT GAA	1011
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ATG GTA AAG	ATC AGT	1053
GGA GGA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAG	TGG GTT	1095
TTG AGA GAG	GGG GAA GAG	TGA			1116
GTCTGAGCAC	GAGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	1166
GCACCTTCCG	GGGCCGCATC	CCTTAGTTTC	CACTGCCTCC	TGTGACGTGA	1216
GGCCCATTTCT	TCACTCTTTG	AAGCGAGCAG	TCAGCATTCT	TAGTAGTGGG	1266
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTA	TTCTTTGTTT	CCTGTTGGAG	1316
TTGTTCAAAT	GTTCTTTTAA	ACGGATGGTT	GAATGAGCGT	CAGCATCCAG	1366
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGAG	1416
TAAGAGTCTT	GttTTTTACT	CAAATTgGGA	AATCCATTCC	ATTTTGTGAA	1466
TTGTGACATA	ATAATAGCAG	TGGTAAAAGT	ATTTGCTTAA	AATTGTGAGC	1516
GAATTAGCAA	TAACATACAT	GAGATAACTC	AAGAAATCAA	AAGATAGTTG	1566
ATTCTTGCCCT	TGTACCTCAA	TCTATTCTGT	AAAATTAAAC	AAATATGCAA	1616

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT      50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG      100
GCCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG      150
AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA      200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC      250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT      300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC      350
CTCTCACTTC CTCCTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC      400
AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG      450
TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC      500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCCCACA      550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                               580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA      622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG      664
CAG GCT CTT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT      706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC      748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC      790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT      832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC      874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG      916
GTG GCC AAG TTG GTT CAT TTT CTG CTC                               943

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(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG      50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC      100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG      150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT      200
TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT      250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA      300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT      350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA      400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC      450

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TGGAGGCCAC	AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTTGT	500
TAGAGCCTCT	AAGATTTGGT	TCTCAGCTGA	GGTCTCTCAC	ATGCTCCCTC	550
TCTCCGTAGG	CCTGTGGGTC	CCCATTGCCC	AGCTTTTGCC	TGCACTCTTG	600
CCTGCTGCCC	TGACCAGAGT	CATC			624
ATG TCT TCT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	666
GGC GTT GAG	GCC CAA GAA	GAG GCC CTG	GGC CTG GTG	GGT GCA	708
CAG GCT CCT	ACT ACT GAG	GAG CAG GAG	GCT GCT GTC	TCC TCC	750
TCC TCT CCT	CTG GTC CCT	GGC ACC CTG	GAG GAA GTG	CCT GCT	792
GCT GAG TCA	GCA GGT CCT	CCC CAG AGT	CCT CAG GGA	GCC TCT	834
GCC TTA CCC	ACT ACC ATC	AGC TTC ACT	TGC TGG AGG	CAA CCC	876
AAT GAG GGT	TCC AGC AGC	CAA GAA GAG	GAG GGG CCA	AGC ACC	918
TCG CCT GAC	GCA GAG TCC	TTG TTC CGA	GAA GCA CTC	AGT AAC	960
AAG GTG GAT	GAG TTG GCT	CAT TTT CTG	CTC CGC AAG	TAT CGA	1002
GCC AAG GAG	CTG GTC ACA	AAG GCA GAA	ATG CTG GAG	AGA GTC	1044
ATC AAA AAT	TAC AAG CGC	TGC TTT CCT	GTG ATC TTC	GGC AAA	1086
GCC TCC GAG	TCC CTG AAG	ATG ATC TTT	GGC ATT GAC	GTG AAG	1128
GAA GTG GAC	CCC GCC AGC	AAC ACC TAC	ACC CTT GTC	ACC TGC	1170
CTG GGC CTT	TCC TAT GAT	GGC CTG CTG	GGT AAT AAT	CAG ATC	1212
TTT CCC AAG	ACA GGC CTT	CTG ATA ATC	GTC CTG GGC	ACA ATT	1254
GCA ATG GAG	GGC GAC AGC	GCC TCT GAG	GAG GAA ATC	TGG GAG	1296
GAG CTG GGT	GTG ATG GGG	GTG TAT GAT	GGG AGG GAG	CAC ACT	1338
GTC TAT GGG	GAG CCC AGG	AAA CTG CTC	ACC CAA GAT	TGG GTG	1380
CAG GAA AAC	TAC CTG GAG	TAC CGG CAG	GTA CCC GGC	AGT AAT	1422
CCT GCG CGC	TAT GAG TTC	CTG TGG GGT	CCA AGG GCT	CTG GCT	1464
GAA ACC AGC	TAT GTG AAA	GTC CTG GAG	CAT GTG GTC	AGG GTC	1506
AAT GCA AGA	GTT CGC ATT	GCC TAC CCA	TCC CTG CGT	GAA GCA	1548
GCT TTG TTA	GAG GAG GAA	GAG GGA GTC	TGA		1578
GCATGAGTTG	CAGCCAGGGC	TGTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC	CCTGTGCAGC	AGCTTCCCTT	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC	TCTGTTTGAA	GAAAATAGTC	AGTGTTCCTTA	GTAGTGGGTT	1728
TCTATTTTGT	TGGATGACTT	GGAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT	TCCTTTTAAT	GGATGGTTGA	ATTAACTTCA	GCATCCAAGT	1828
TTATGAATCG	TAGTTAACGT	ATATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT	TTTATTCAGA	TTGGGAAATC	CGTTCTATTT	TGTGAATTTG	1928
GGACATAATA	ACAGCAGTGG	AGTAAGTATT	TAGAAGTGTG	AATTCACCGT	1978
GAAATAGGTG	AGATAAATTA	AAAGATACTT	AATTCCTGCC	TTATGCCTCA	2028
GTCTATTCTG	TAAAATTTAA	AAATATATAT	GCATACCTGG	ATTTCTTTGG	2078
CTTCGTGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAATAATT	CTTTCTGTTA	2128
ACTGGCTCAT	TTCTTCTCTA	TGCACTGAGC	ATCTGCTCTG	TGGAAGGCCC	2178
AGGATTAGTA	GTGGAGATAC	TAGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG	AGTCTAGGAG	CGCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT	GTAGGGGAAA	AGTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC	GGGTGTAAAT	TCCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTGCATTT	TCTTCTGAGG	GATCTGATTC	TAATGAAGCT	TGGTGGGTCC	2428
AGGGCCAGAT	TCTCAGAGGG	AGAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478
TCTGAGCAGT	TCCTTTGTGA	CAATGGATGA	ACAGAGAGGA	GCCTCTACCT	2528
GGG					2531

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-41 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC	CCTGCCTGGA	GAAATGTGAG	GGCCCTGAGT	GAACACAGTG	50
GGGATCATCC	ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100
TCTTGATGGC	ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCTAAG	150
GGCCCATGGA	TTCCTCTCCT	AGGAGCTCCA	GGAACAAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTGTCTCT	AGGTTACAGA	GCAGAGGATG	CACAGGCTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAAGACACAT	AGGACTCCAA	AGAGTCTGGC	CTCACCTCCC	TACCATCAAT	350
CCTGCAGAAT	CGACCTCTGC	TGGCCGGCTA	TACCCTGAGG	TGCTCTCTCA	400
CTTCCTCCTT	CAGGTTCTGA	GCAGACAGGC	CAACCGGAGA	CAGGATTCCC	450
TGGAGGCCAC	AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTTGT	500
TAGAGCCTCT	AAGATTGGT	TCTCAGTTGA	GGTCTCTCAC	ATGCTCCCTC	550
TCTCCGTAGG	CCTGTGGGTC	CCCATTGCC	AGCTTTTGCC	TGCACTCTTG	600
CCTGCTGCCC	TGAGCAGAGT	CATC			624
ATG TCT TCT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	666
GGC GTT GAG	GCC CAA GAA	GAG GCC CTG	GGC CTG GTG	GGT GCG	708
CAG GCT CCT	ACT ACT GAG	GAG CAG GAG	GCT GCT GTC	TCC TCC	750
TCC TCT CCT	CTG GTC CCT	GGC ACC CTG	GAG GAA GTG	CCT GCT	792
GCT GAG TCA	GCA GGT CCT	CCC CAG AGT	CCT CAG GGA	GCC TCT	834
GCC TTA CCC	ACT ACC ATC	AGC TTC ACT	TGC TGG AGG	CAA CCC	876
AAT GAG GGT	TCC AGC AGC	CAA GAA GAG	GAG GGG CCA	AGC ACC	918
TCG CCT GAC	GCA GAG TCC	TTG TTC CGA	GAA GCA CTC	AGT AAC	960
AAG GTG GAT	GAG TTG GCT	CAT TTT CTG	CTC CGC AAG	TAT CGA	1002
GCC AAG GAG	CTG GTC ACA	AAG GCA GAA	ATG CTG GAG	AGA GTC	1044
ATC AAA AAT	TAC AAG CGC	TGC TTT CCT	GTG ATC TTC	GGC AAA	1086
GCC TCC GAG	TCC CTG AAG	ATG ATC TTT	GGC ATT GAC	GTG AAG	1128
GAA GTG GAC	CCC ACC AGC	AAC ACC TAC	ACC CTT GTC	ACC TGC	1170
CTG GGC CTT	TCC TAT GAT	GGC CTG CTG	GGT AAT AAT	CAG ATC	1212
TTT CCC AAG	ACA GGC CTT	CTG ATA ATC	GTC CTG GGC	ACA ATT	1254
GCA ATG GAG	GGC GAC AGC	GCC TCT GAG	GAG GAA ATC	TGG GAG	1296
GAG CTG GGT	GTG ATG GGG	GTG TAT GAT	GGG AGG GAG	CAC ACT	1338
GTC TAT GGG	GAG CCC AGG	AAA CTG CTC	ACC CAA GAT	TGG GTG	1380
CAG GAA AAC	TAC CTG GAG	TAC CGG CAG	GTA CCC GGC	AGT AAT	1422
CCT GCG CGC	TAT GAG TTC	CTG TGG GGT	CCA AGG GCT	CTG GCT	1464
GAA ACC AGC	TAT GTG AAA	GTC CTG GAG	CAT GTG GTC	AGG GTC	1506
AAT GCA AGA	GTT CGC ATT	GCC TAC CCA	TCC CTG CGT	GAA GCA	1548
GCT TTG TTA	GAG GAG GAA	GAG GGA GTC	TGA		1578
GCATGAGTTG	CAGCCAGGGC	TGTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC	CCTGTGCAGC	AGCTTCCCTT	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC	TCTGTTTGAA	GAAAATAGTC	AGTGTTCTTA	GTAGTGGGTT	1728
TCTATTTTGT	TGGATGACTT	GGAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT	TCCTTTTAAT	GGATGGTTGA	ATTAAC TTCA	GCATCCAAGT	1828
TTATGAATCG	TAGTTAACGT	ATATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT	TTTATTTCAG	TTGGGAAATC	CGTTCTATTT	TGTGAATTTG	1928
GGACATAATA	ACAGCAGTGG	AGTAAGTATT	TAGAAGTGTG	AATTCACCGT	1978
GAAATAGGTG	AGATAAATTA	AAAGATACTT	AATTCCTGCC	TTATGCCTCA	2028
GTCTATTCTG	TAAAATTTAA	AAATATATAT	GCATACCTGG	ATTTCTTTGG	2078
CTTCGTGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAATAATT	CTTTCTGTTA	2128
ACTGGCTCAT	TTCTTCTCTA	TGCACTGAGC	ATCTGCTCTG	TGGAAGGCC	2178
AGGATTAGTA	GTGGAGATAC	TAGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG	AGTCTAGGAG	CGCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT	GTAGGGGAAA	AGTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC	GGGTGTAAAT	TCCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTCCATTT	TCTTCTGAGG	GATCTGATTC	TAATGAAGCT	TGGTGGGTCC	2428
AGGGCCAGAT	TCTCAGAGGG	AGAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478

TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT 2528
 GGG 2531

(2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	770
GCCCATCTCT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG	820
GTTTCTATTT TGTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	870
ATTGTTGAAA TGTTCCCTTT AATGGATGGT TGAATTAAT TCAGCATCCA	920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1068

(2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG	50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC	100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG	150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT	200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC	250

TAGTGCCAGC	AGTGAACGTT	TGCCTTGAAT	GCACACTAAT	GGCCCCCATC	300
GGCCCAGAAC	ATATGGGACT	CCAGAGCACC	TGGCCTCACC	CTCTCTACTG	350
TCAGTCCTGC	AGAATCAGCC	TCTGCTTGCT	TGTGTACCCT	GAGGTGCCCT	400
CTCACTTTTT	CCTTCAGGTT	CTCAGGGGAC	AGGCTGACCA	GGATCACCAG	450
GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTTCAGT	TTTTAGCTGA	550
GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
ATG TCT CTT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	686
CTC CTC TGG	TCC CAG GCA	CCC TGG GGG	AGG TGC CTG	CTG CTG CTG	728
GGT CAC CAG	GTC CTC TCA	AGA GTC CTC	AGG GAG CCT	CCG CCA	770
TCC CCA CTG	CCA TCG ATT	TCA CTC TAT	GGA GGC AAT	CCA TTA	812
AGG GCT CCA	GCA ACC AAG	AAG AGG AGG	GGC CAA GCA	CCT CCC	854
CTG ACC CAG	AGT CTG TGT	TCC GAG CAG	CAC TCA GTA	AGA AGG	896
TGG CTG ACT	TGA				908
TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCTGGT	CACAAAAGGCA	958
GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCTTGAGAT	1008
CTTCGGCAAA	GCCTCCGAGT	CCTTGACAGT	GGTCTTTGGC	ATTGACGTGA	1058
AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1108
CTCCTATGAT	GGCCTGCTGG	TTGATAATAA	TCAGATCATG	CCCAAGACGG	1158
GCCTCCTGAT	AATCGTCTTG	GGCATGATTG	CAATGGAGGG	CAAATGCGTC	1208
CCTGAGGAGA	AAATCTGGGA	GGAGCTGAGT	GTGATGAAGG	TGTATGTTGG	1258
GAGGGAGCAC	AGTGTCTGTG	GGGAGCCCAG	GAAGCTGCTC	ACCCAAGATT	1308
TGGTGCAGGA	AAACTACCTG	GAGTACCGGC	AGGTGCCCAG	CAGTGATCCC	1358
ATATGCTATG	AGTTACTGTG	GGGTCCAAGG	GCACTCGCTG	CTTGAAAAGTA	1408
CTGGAGCACG	TGGTCAGGGT	CAATGCAAGA	GTTCTCATTT	CCTACCCATC	1458
CCTGCGTGAA	GCAGCTTTGA	GAGAGGAGGA	AGAGGGAGTC	TGAGCATGAG	1508
CTGCAGCCAG	GGCCACTGCG	AGGGGGGCTG	GGCCAGTGCA	CCTTCCAGGG	1558
TCCCGTCCAG	TAGTTTCCCC	TGCCTTAATG	TGACATGAGG	CCCATTCCTC	1608
TCTCTTTGAA	GAGAGCAGTC	AACATTCTTA	GTAGTGGGTT	TCTGTTCTAT	1658
TGGATGACTT	TGAGATTTGT	CTTTGTTTCC	TTTGGAATT	GTTCAAATGT	1708
TTCTTTTAAT	GGGTGGTTGA	ATGAACTTCA	GCATTCAAAT	TTATGAATGA	1758
CAGTAGTCAC	ACATAGTGCT	GTTTATATAG	TTTAGGAGTA	AGAGTCTTGT	1808
TTTTTATTCA	GATTGGGAAA	TCCATTCCAT	TTTGTGAATT	GGGACATAGT	1858
TACAGCAGTG	GAATAAGTAT	TCATTTAGAA	ATGTGAATGA	GCAGTAAAC	1908
TGATGACATA	AAGAAATTAA	AAGATATTTA	ATTCTTGCTT	ATACTCAGTC	1958
TATTCGGTAA	AATTTTTTTTT	AAAAAATGTG	CATACCTGGA	TTTCCTTGGC	2008
TTCTTTGAGA	ATGTAAGACA	AATTAAATCT	GAATAAATCA	TTCTCCCTGT	2058
TCACTGGCTC	ATTTATTCTC	TATGCACTGA	GCATTTGCTC	TGTGGAAGGC	2108
CCTGGGTTAA	TAGTGGAGAT	GCTAAGGTAA	GCCAGACTCA	CCCCAACCA	2158
CAGGGTAGTA	AAGTCTAGGA	GCAGCAGTCA	TATAATTAA	GTGGAGAGAT	2208
GCCCTCTAAG	ATGTAGAG				2226

(2) INFORMATION FOR SEQUENCE ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-51 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC	CTTGCCAGGA	GAAAGGTGAG	GGCCCTGTGT	GAGCACAGAG	50
GGGACCATTTC	ACCCCAAGAG	GGTGGAGACC	TCACAGATTC	CAGCCTACCC	100

TCCTGTTAGC	ACTGGGGGCC	TGAGGCTGTG	CTTGCACTCT	GCACCCTGAG	150
GGCCCATGCA	TTCCTCTTCC	AGGAGCTCCA	GGAAACAGAC	ACTGAGGCCT	200
TGGTCTGAGG	CCGTGCCCTC	AGGTCACAGA	GCAGAGGAGA	TGCAGACGTC	250
TAGTGCCAGC	AGTGAACGTT	TGCCTTGAAT	GCACACTAAT	GGCCCCCATC	300
GGCCCAAGAA	ATATGGGACT	CCAGAGCACC	TGGCCTCACC	CTCTCTACTG	350
TCAGTCCTGC	AGAATCAGCC	TCTGCTTGCT	TGTGTACCCT	GAGGTGCCCT	400
CTCACTTTTT	CCTTCAGGTT	CTCAGGGGAC	AGGCTGACCA	GGATCACCAG	450
GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTCACT	TTTGTAGCTGA	550
GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
ATG TCT CTT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	686
GGC CTT GAC	ACC CAA GAA	GAG CCC TGG	GCC TGG TGG	GTG TGC	728
AGG CTG CCA	CTA CTG AGG	AGC AGG AGG	CTG TGT CCT	CCT CCT	770
CTC CTC TGG	TCC CAG GCA	CCC TGG GGG	AGG TGC CTG	CTG CTG	812
GGT CAC CAG	GTC CTC TCA	AGA GTC CTC	AGG GAG CCT	CCG CCA	854
TCC CCA CTG	CCA TCG ATT	TCA CTC TAT	GGA GGC AAT	CCA TTA	896
AGG GCT CCA	GCA ACC AAG	AAG AGG AGG	GGC CAA GCA	CCT CCC	938
CTG ACC CAG	AGT CTG TGT	TCC GAG CAG	CAC TCA GTA	AGA AGG	980
TGG CTG ACT	TGA				992
TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCCGGT	CACAAAGGCA	1042
GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCCTGAGAT	1092
CTTCGGCAAA	GCCTCCGAGT	CCTTGCAGCT	GGTCTTTGGC	ATTGACGTGA	1142
AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1192
CTCCTATGAT	GGCCTGGTGG	TTTAATCAGA	TCATGCCCAA	GACGGGCCTC	1242
CTGATAATCG	TCTTGGGCAT	GATTGCAATG	GAGGGCAAAT	GCGTCCCTGA	1292
GGAGAAAATC	TGGGAGGAGC	TGGGTGTGAT	GAAGGTGTAT	GTTGGGAGGG	1342
AGCACAGTGT	CTGTGGGGAG	CCCAGGAAGC	TGCTCACCCA	AGATTTGGTG	1392
CAGGAAAAC	ACCTGGAGTA	CCGCAGGTGC	CCAGCAGTGA	TCCCATATGC	1442
TATGAGTTAC	TGTGGGGTCC	AAGGGCACTC	GCTGCTTGAA	AGTACTGGAG	1492
CACGTGGTCA	GGGTCAATGC	AAGAGTTCTC	ATTTCTTACC	CATCCCTGCA	1542
TGAAGCAGCT	TTGAGAGAGG	AGGAAGAGGG	AGTCTGAGCA	TGAGCTGCAG	1592
CCAGGGCCAC	TGCGAGGGGG	GCTGGGCCAG	TGCACCTTCC	AGGGCTCCGT	1642
CCAGTAGTTT	CCCCTGCCTT	AATGTGACAT	GAGGCCCAT	CTTCTCTCTT	1692
TGAAGAGAGC	AGTCAACATT	CTTAGTAGTG	GGTTTCTGTT	CTATTGGATG	1742
ACTTTGAGAT	TTGTCTTTGT	TTCTTTTGG	AATTGTTCAA	ATGTTCCCTT	1792
TAATGGGTGG	TTGAATGAAC	TTCAGCATT	AAATTTATGA	ATGACAGTAG	1842
TCACACATAG	TGCTGTTTAT	ATAGTTTAGG	AGTAAGAGTC	TTGTTTTTTA	1892
TTCAGATTGG	GAAATCCATT	CCATTTTGTG	AATTGGGACA	TAGTTACAGC	1942
AGTGAATAAA	GTATTCATTT	AGAAATGTGA	ATGAGCAGTA	AACTGATGA	1992
GATAAAGAAA	TTAAAGATA	TTTAATTCTT	GCCTTATACT	CAGTCTATTC	2042
GGTAAATTTT	TTTTTTAAAA	ATGTGCATAC	CTGGATTTC	TTGGCTTCTT	2092
TGAGAATGTA	AGACAAATTA	AATCTGAATA	AATCATTCTC	CCTGTTCACT	2142
GGCTCATTTA	TTCTCTATGC	ACTGAGCATT	TGCTCTGTGG	AAGGCCCTGG	2192
GTTAATAGTG	GAGATGCTAA	GGTAAGCCAG	ACTCACCCCT	ACCCACAGGG	2242
TAGTAAAGTC	TAGGAGCAGC	AGTCATATAA	TTAAGGTGGA	GAGATGCCCT	2292
CTAAGATGTA	GAG				2305

(2) INFORMATION FOR SEQUENCE ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-6 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
TGT GCC CCT GAG GAG	225

(2) INFORMATION FOR SEQUENCE ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-7 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA	50
GAGCCCAGCC TCACCTTCCC TACTGTCACT CCTGCAGCCT CAGCCTCTGC	100
TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCTCTCCTT CAGGTTCTCA	150
GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC	200
ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT	250
GGTTCACAAA TGAGGCCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG	300
GTTCTCTCCC ATCGCCAGC TGCTGCCCCG ACTCCAGCCT GCTGCCCTGA	350
CCAGAGTCAT CATGCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG	400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG	450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA	500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA	550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA	600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC	650
TAGACACACC CCGCTCACCT GGCCTCCTTG TTCCA	685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT	727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA	769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT	811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC	853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA	895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC	937
AGA GCA TGC CCG AGA CCG GCC TTC TGA	964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG	1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT	1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC	1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCACTT	1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG	1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCCTA CCCATCCCTG	1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC	1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC	1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT	1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG	1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC	1514
GATTTGGAGG TTTATCTTTG TTTCTTTTGG CAGTCGTTCA AATGTTCTCT	1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTTCATGT ATGACAGTAG	1614
GCAGACTTAC TGTTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTTAT	1664

TTATGTAAGA	AAATCTATGT	TATTTCTTGA	ATTGGGACAA	CATAACATAG	1714
CAGAGGATTA	AGTACCTTTT	ATAATGTGAA	AGAACAAAGC	GGTAAAATGG	1764
GTGAGATAAA	GAAATAAAGA	AATTAAATTG	GCTGGGCACG	GTGGCTCACG	1814
CCTGTAATCC	CAGCACTTTA	GGAGGCAGAG	GCACGGGGAT	CACGAGGTCA	1864
GGAGATCGAG	ACCATTCTGG	CTAACACAGT	GAAACACCAT	CTCTATTAAA	1914
AATACAAAAC	TTAGCCGGGC	GTGGTGGCGG	GTG		1947

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-8 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG	AACCAGGCTG	TGAGGTCTTG	GTCTGAGGCA	GTATCTTCAA	50
TCACAGAGCA	TAAGAGGCCC	AGGCAGTAGT	AGCAGTCAAG	CTGAGGTGGT	100
GTTTCCCCTG	TATGTATACC	AGAGGCCCTT	CTGGCATCAG	AACAGCAGGA	150
ACCCACAGT	TCCTGGCCCT	ACCAGCCCTT	TTGTCAGTCC	TGGAGCCTTG	200
GCCTTTGCCA	GGAGGCTGCA	CCCTGAGATG	CCCTCTCAAT	TTCTCCTTCA	250
GGTTGCGAGA	GAACAGGCCA	GCCAGGAGGT	CAGGAGGCCC	CAGAGAAGCA	300
CTGAAGAAGA	CCTGTAAGTA	GACCTTTGTT	AGGGCATCCA	GGGTGTAGTA	350
CCCAGCTGAG	GCCTCTCACA	CGCTTCCTCT	CTCCCCAGGC	CTGTGGGTCT	400
CAATTGCCCA	GCTCCGGCCC	ACACTCTCCT	GCTGCCCTGA	CCTGAGTCAT	450
C					451
ATG CTT CTT	GGG CAG AAG	AGT CAG CGC	TAC AAG GCT	GAG GAA	493
GGC CTT CAG	GCC CAA GGA	GAG GCA CCA	GGG CTT ATG	GAT GTG	535
CAG ATT CCC	ACA GCT GAG	GAG CAG AAG	GCT GCA TCC	TCC TCC	577
TCT ACT CTG	ATC ATG GGA	ACC CTT GAG	GAG GTG ACT	GAT TCT	619
GGG TCA CCA	AGT CCT CCC	CAG AGT CCT	GAG GGT GCC	TCC TCT	661
TCC CTG ACT	GTC ACC GAC	AGC ACT CTG	TGG AGC CAA	TCC GAT	703
GAG GGT TCC	AGC AGC AAT	GAA GAG GAG	GGG CCA AGC	ACC TCC	745
CCG GAC CCA	GCT CAC CTG	GAG TCC CTG	TTC CGG GAA	GCA CTT	787
GAT GAG AAA	GTG GCT GAG	TTA GTT CGT	TTC CTG CTC	CGC AAA	829
TAT CAA ATT	AAG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTT GAG	871
AGT GTC ATC	AAA AAT TAC	AAG AAC CAC	TTT CCT GAT	ATC TTC	913
AGC AAA GCC	TCT GAG TGC	ATG CAG GTG	ATC TTT GGC	ATT GAT	955
GTG AAG GAA	GTG GAC CCT	GCC GGC CAC	TCC TAC ATC	CTT GTC	997
ACC TGC CTG	GGC CTC TCC	TAT GAT GGC	CTG CTG GGT	GAT GAT	1039
CAG AGT ACG	CCC AAG ACC	GGC CTC CTG	ATA ATC GTC	CTG GGC	1081
ATG ATC TTA	ATG GAG GGC	AGC CGC GCC	CCG GAG GAG	GCA ATC	1123
TGG GAA GCA	TTG AGT GTG	ATG GGG GCT	GTA TGA		1156
TGGGAGGGAG	CACAGTGTCT	ATTGGAAGCT	CAGGAAGCTG	CTCACCCAAG	1206
AGTGGGTGCA	GGAGAACTAC	CTGGAGTACC	GCCAGGCGCC	CGGCAGTGAT	1256
CCTGTGCGCT	ACGAGTTTCT	GTGGGGTCCA	AGGGCCCTTG	CTGAAACCAG	1306
CTATGTGAAA	GTCCTGGAGC	ATGTGGTCAG	GGTCAATGCA	AGAGTTCGCA	1356
TTTCCTACCC	ATCCCTGCAT	GAAGAGGCTT	TGGGAGAGGA	GAAAGGAGTT	1406
TGAGCAGGAG	TTGCAGCTAG	GGCCAGTGGG	GCAGGTTGTG	GGAGGGCCTG	1456
GGCCAGTGCA	CGTTCCAGGG	CCACATCCAC	CACTTTCCCT	GCTCTGTTAC	1506
ATGAGGCCCA	TTCTTCACTC	TGTGTTTGAA	GAGAGCAGTC	ACAGTTCTCA	1556
GTAGTGGGGA	GCATGTTGGG	TGTGAGGGAA	CACAGTGTGG	ACCATCTCTC	1606
AGTTCTTGTT	CTATTGGGCG	ATTTGGAGGT	TTATCTTTGT	TTCTTTTGG	1656
AATTGTTCCA	ATGTTCTTTC	TAATGGATGG	TGTAATGAAC	TTCAACATTC	1706

ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA	1756
GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA	1806
ATTC	1810

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-9 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC	50
AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT	100
GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG	150
TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC	200
TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA	250
GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT	300
TGTTAGAACC TCCAAGGTTT GGTTCACGC TGAAGTCTCT CACACACTCC	350
CTCTCTCCCC AGGCCGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC	400
CTGACTGCTG CCCTGACCAG AGTCATC	427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA	469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA	511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT	553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT	595
CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC	637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC	679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT	721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG	763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG	805
GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA	847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC	889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG	931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC	973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC	1015
AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC	1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG	1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC	1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA	1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG	1225
CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC	1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA	1309
AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG	1351
GGA GAG GAG CAA GAG GGA GTC TGA	1375
GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA	1412

(2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-10 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA    50
CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT    100
CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA    150
AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT    200
GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA    250
CCCTCCCTCT CTCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC    300
ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC                      333
ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA    375
GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA    417
CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT    459
TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC    501
TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC    543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC    585
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT    627
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA    669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT    711
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT    753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG    795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT    837
GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC    879
ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC    920

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(2) INFORMATION FOR SEQUENCE ID NO: 23:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (ix) FEATURE:
 (A) NAME/KEY: MAGE-11 gene
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT    50
CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT    100
CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG    150
GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG    200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG    250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC    300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC    350
ACTCTAGAGG AGTTGCCCTG TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC    400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC    450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG    500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA    550
GATAATTGAT TTGGTTCAAT TATTCTCCGC AAGTATCGAG TCAAGGGGCT    600
GATCACAAG GCAGAA                      616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT    658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT    700
GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT    742
GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG    784
TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA    826

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GTC	CTG	GGT	GTA	ATC	TTC	ATG	GAG	GGG	AAC	TGC	ATC	CCT	GAA	868
GAG	GTT	ATG	TGG	GAA	GTC	CTG	AGC	ATT	ATG	GGG	GTG	TAT	GCT	910
GGA	AGG	GAG	CAC	TTC	CTC	TTT	GGG	GAG	CCC	AAG	AGG	CTC	CTT	952
ACC	CAA	AAT	TGG	GTG	CAG	GAA	AAG	TAC	CTG	GTG	TAC	CGG	CAG	994
GTG	CCC	GGC	ACT	GAT	CCT	GCA	TGC	TAT	GAG	TTC	CTG	TGG	GGT	1036
CCA	AGG	GCC	CAC	GCT	GAG	ACC	AGC	AAG	ATG	AAA	GTT	CTT	GAG	1078
TAC	ATA	GCC	AAT	GCC	AAT	GGG	AGG	GAT	CC					1107

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AGAGTTCATA	GCCTACCAGA	ACCAACATGC	ATCCATTCTT	GGCCTGTTAT	1637
ACATTAGTAG	AATGGAGGCT	ATTTTTGTTA	CTTTTCAAAT	GTTTGTTTAA	1687
CTAAACAGTG	CTTTTTGCCA	TGCTTCTTGT	TAACTGCATA	AAGAGGTAAC	1737
TGTCACTTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTCATG	GCAATGTGAT	ATCATACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: smage-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCCCTA	400
GAAAGATGTT	CTCCTGGAAG	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCCTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTTCAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCCCT	ATTTGCTGGT	AGGCAAACTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACCTGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCCCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AAGGGTGTTT	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTGTTC	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600

AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTG	1750
TCACTTGTC	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACTCTA	TTACTTTATT	2050
ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

- (2) INFORMATION FOR SEQUENCE ID NO: 26:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acids
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
5

- (2) INFORMATION FOR SEQUENCE ID NO: 27:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ACTCAGCTCC TCCCAGATTT 20

- (2) INFORMATION FOR SEQUENCE ID NO: 28:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAAGAGGAGG GGCCAAG 17

- (2) INFORMATION FOR SEQUENCE ID NO: 29:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCTTGTATCC TGGAGTCC 18

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGCCAAGAT CTCAGGAA

18